

THE MICROBIAL DIVERSITY OF HIGH-ALTITUDE GEOTHERMAL SPRINGS OF ARMENIA AND NAGORNO-KARABAKH

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The microbial diversity of nine high-altitude geothermal springs (T 25.8–70°C, pH 6.0–7.5, total mineralization of 0.5 mg/L) located on the Armenian Highland has been recently assessed to explore their biotechnological potential. All these geothermal springs are at altitudes ranging from 960–2090 m above sea level and are located on the Alpide (Alpine–Himalayan) orogenic belt, a seismically active region. The taxonomic diversity of hot spring microbiomes has been examined using culture-independent approaches, including denaturing gradient gel electrophoresis (DGGE), 16S rRNA gene library construction, 454 pyrosequencing, and Illumina HiSeq. The bacterial phyla Proteobacteria, Bacteroidetes, Cyanobacteria, and Firmicutes are the predominant life forms in the studied springs. Archaea mainly include the phyla Euryarchaeota, Crenarchaeota, and Thaumarchaeota, and comprise less than 1% of the prokaryotic community. Temperature seems to be an important factor in shaping the microbial communities of these springs. Overall, the diversity and richness of the microbiota are negatively affected by increasing temperature. Other abiotic factors, including pH, mineralization, and geological history, also impact the structure and function of the microbial community. More than 130 bacterial and archaeal strains (*Bacillus*, *Geobacillus*, *Parageobacillus*, *Anoxybacillus*, *Paenibacillus*, *Brevibacillus*, *Aeribacillus*, *Ureibacillus*, *Thermoactinomyces*, *Sporosarcina*, *Thermus*, *Rhodobacter*, *Thiospirillum*, *Thiocapsa*, *Rhodopseudomonas*, *Methylocaldum*, *Desulfomicrobium*, *Desulfovibrio*, *Treponema*, *Arcobacter*, *Nitrospira*, and *Methanoculleus*) have been reported, some of which may be representative of novel species (sharing 91–97% sequence identity with their closest matches in GenBank) and producers of thermozymes and biomolecules with potential biotechnological applications. Whole-genome shotgun sequencing of *T. scotoductus* K1, as well as of the potentially new *Treponema* sp. J25 and *Anoxybacillus* sp. K1, were performed. Detailed characterization of thermophilic isolates indicate the potential of the studied springs as a source of biotechnologically valuable microbes and biomolecules.